



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/779,476

DATE: 07/27/2004

TIME: 12:56:00

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Output Set: N:\CRF4\07272004\J779476.raw

3 <110> APPLICANT: Salmedix, Inc.  
 4 Leoni, Lorenzo M.  
 6 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION AND TREATMENT OF  
 7 METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENT CANCERS  
 9 <130> FILE REFERENCE: 076936-0307942  
 11 <140> CURRENT APPLICATION NUMBER: 10/779,476  
 12 <141> CURRENT FILING DATE: 2004-02-13  
 14 <150> PRIOR APPLICATION NUMBER: 60/447,888  
 15 <151> PRIOR FILING DATE: 2003-02-14  
 17 <150> PRIOR APPLICATION NUMBER: 60/460,715  
 18 <151> PRIOR FILING DATE: 2004-04-04  
 20 <160> NUMBER OF SEQ ID NOS: 12  
 22 <170> SOFTWARE: PatentIn version 3.2  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 283  
 26 <212> TYPE: PRT  
 27 <213> ORGANISM: Homo sapiens  
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 36 20 25 30  
 39 Tyr Val Asp Thr Pro Phe Gly Lys Pro Ser Asp Ala Leu Ile Leu Gly  
 40 35 40 45  
 43 Lys Ile Lys Asn Val Asp Cys Ile Leu Leu Ala Arg His Gly Arg Gln  
 44 50 55 60  
 47 His Thr Ile Met Pro Ser Lys Val Asn Tyr Gln Ala Asn Ile Trp Ala  
 48 65 70 75 80  
 51 Leu Lys Glu Glu Gly Cys Thr His Val Ile Val Thr Thr Ala Cys Gly  
 52 85 90 95  
 55 Ser Leu Arg Glu Glu Ile Gln Pro Gly Asp Ile Val Ile Ile Asp Gln  
 56 100 105 110  
 59 Phe Ile Asp Arg Thr Thr Met Arg Pro Gln Ser Phe Tyr Asp Gly Ser  
 60 115 120 125  
 63 His Ser Cys Ala Arg Gly Val Cys His Ile Pro Met Ala Glu Pro Phe  
 64 130 135 140  
 67 Cys Pro Lys Thr Arg Glu Val Leu Ile Glu Thr Ala Lys Lys Leu Gly  
 68 145 150 155 160  
 71 Leu Arg Cys His Ser Lys Gly Thr Met Val Thr Ile Glu Gly Pro Arg  
 72 165 170 175  
 75 Phe Ser Ser Arg Ala Glu Ser Phe Met Phe Arg Thr Trp Gly Ala Asp  
 76 180 185 190  
 79 Val Ile Asn Met Thr Thr Val Pro Glu Val Val Leu Ala Lys Glu Ala



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83 Gly Ile Cys Tyr Ala Ser Ile Ala Met Ala Thr Asp Tyr Asp Cys Trp
84          210          215          220
87 Lys Glu His Glu Glu Ala Val Ser Val Asp Arg Val Leu Lys Thr Leu
88 225          230          235          240
91 Lys Glu Asn Ala Asn Lys Ala Lys Ser Leu Leu Leu Thr Thr Ile Pro
92          245          250          255
95 Gln Ile Gly Ser Thr Glu Trp Ser Glu Thr Leu His Asn Leu Lys Asn
96          260          265          270
99 Met Ala Gln Phe Ser Val Leu Leu Pro Arg His
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104 <211> LENGTH: 2269
105 <212> TYPE: DNA
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113 catggcctct ggcaccacca ccaccgcgct gaagattgga ataattggtg gaacaggcct 180
115 gcatgatcca gaaattttag aaggaagaac tgaaaaatat gtggatactc catttggcaa 240
117 gccatctgat gccttaattt tggggaagat aaaaaatgtt gattgcatcc tccttgcaag 300
119 gcatggaagg cagcacacca tcatgccttc aaaggtcaac taccaggcga acatctgggc 360
121 tttgaaggaa gagggctgta cacatgtcat agtgaccaca gcttgtggct ccttgaggga 420
123 ggagattcag cccggcgata ttgtcattat tgatcagttc attgacagga ccactatgag 480
125 acctcagtc ttctatgatg gaagtcattc ttgtgccaga ggagtgtgcc atattccaat 540
127 ggctgagccg ttttgcccca aaacgagaga gggtcttata gagactgcta agaagctagg 600
129 actccggtgc cactcaaagg ggacaatggt cacaatcgag ggacctcgtt ttagctcccg 660
131 ggcagaaagc ttcatgttcc gcacctgggg ggcggtgtt atcaacatga ccacagttcc 720
133 agaggtggtt cttgctaagg aggctggaat ttgttacgca agtatcgcca tggcgacaga 780
135 ttatgactgc tggaaggagc acgaggaagc agtttcggtg gaccgggtct taaagaccct 840
137 gaaagaaaac gctaataaag ccaaaagctt actgctcact accatacctc agatagggtc 900
139 cacagaatgg tcagaaaccc tccataacct gaagaatatg gcccgatttt ctgttttatt 960
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143 ttttgggaat tctgtcttaa cttgaaaaaa atatgggaaa gacatgcagc tttcatgccc 1080
145 ttgcctatca aagagtatgt tgtaagaaag acaagacatt gtgtgtatta gagactcctg 1140
147 aatgatttag acaacttcaa aatacagaag aaaagcaaat gactagtata catgtgggaa 1200
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161 atcccttgca attggaggtg aattatgtct tagttataat ctagattgtg aatcagccaa 1620
163 ctgaaaatcc tttttgcata tttcaatgtc ctaaaaagac acggttgctc tatatatgaa 1680
165 gtgaaaaaag gatatggtag cattttatag tactagtttt gctttaaaat gctatgtaaa 1740
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169 ctgggataat ttttattttc tttgaatctt tctgtgtctt cacatttttc tacagtgaat 1860
171 ataatacaat agtaaagggc cgtaaaaata aaagtggatt tagaaaagatc cagttcttga 1920
173 aaacactgtt tctggtaatg aagcagaatt taagttggta atattaagggt gaatgtcatt 1980

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175 taagggaggtt acatctttat tctgctaaag aagaggatca ttgatttctg tacagtcaga 2040
177 acagtacttg ggtgtgcaac agctttctga gaaaagctag gtgtataata gtttaactga 2100
179 aagtttaact atttaaaaga ctaaatgcac attttatggt atctgatatt ttaaaaagta 2160
181 atgtgagctt ctccttttta tgagttaaat tattttatac gagttggtaa tttgtgcctt 2220
183 ttaataaagt ggaagcttgc tttttaaaaa aaaaaaaaaa gcggaattc 2269
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188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 3
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194 1 5 10 15
197 Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
198 20 25 30
201 Glu Ala Gly Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
202 35 40 45
205 Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
206 50 55 60
209 Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
210 65 70 75 80
213 Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
214 85 90 95
217 Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
218 100 105 110
221 Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
222 115 120 125
225 Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
226 130 135 140
229 Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
230 145 150 155
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234 <211> LENGTH: 1218
235 <212> TYPE: DNA
236 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 4
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241 tcctccgagc actcgtcac ggctcccct tgcttgaaa gataccgcgg tccctccaga 120
243 ggatttgagg gacagggctc gagggggctc ttccgccagc accggaggaa gaaagaggag 180
245 gggctggctg gtcaccagag ggtggggcgg accgctgctg ctccggcggt gcggagaggg 240
247 ggagagcagg cagcggggcg cggggagcag catggagccg gcggcgggga gcagcatgga 300
249 gccttcggct gactggctgg ccacggccgc ggcccggggt cgggtagagg aggtgcgggc 360
251 gctgctggag gcgggggcgc tgcccaacgc accgaatagt tacggtcggg gcccgatcca 420
253 ggtcatgatg atgggcagcg cccgagtggc ggagctgctg ctgctccacg gcgcggagcc 480
255 caactgcgcc gaccccgcca ctctcaccgc acccgtgcac gacgctgccc gggagggcct 540
257 cctggacacg ctggtggtgc tgcaccgggc cggggcgcg ctggacgtgc gcgatgcctg 600
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261 gcgcgcggct gcggggggca ccagaggcag taacctatgc cgcgatagtg ccgcggaagg 720
263 tccctcagac atccccgatt gaaagaacca gagaggctct gagaaacctc gggaaactta 780
265 gatcatcagt caccgaaggt cctacagggc cacaactgcc cccgccacaa cccaccccg 840

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267 tttcgtagtt ttcatttaga aaatagagct tttaaaaaatg tcctgccttt taacgtagat      900
269 atatgccttc cccactacc gtaaagtgtcc atttatatca ttttttataat attccttataa      960
271 aaatgtaaaa aagaaaaaca ccgcttctgc cttttcactg tgttgagggtt ttctggagtg      1020
273 agcactcacg ccctaagcgc acattcatgt gggcatttct tgcgagcctc gcagcctccg      1080
275 gaagctgtcg acttcatgac aagcattttg tgaactaggg aagctcaggg gggttactgg      1140
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283 <211> LENGTH: 173
284 <212> TYPE: PRT
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294                20                    25                    30
297 Glu Leu Gly Pro Gly Gly Gly Glu Asn Met Val Arg Arg Phe Leu Val
298                35                    40                    45
301 Thr Leu Arg Ile Arg Arg Ala Cys Gly Pro Pro Arg Val Arg Val Phe
302                50                    55                    60
305 Val Val His Ile Pro Arg Leu Thr Gly Glu Trp Ala Ala Pro Gly Ala
306 65                70                    75                    80
309 Pro Ala Ala Val Ala Leu Val Leu Met Leu Leu Arg Ser Gln Arg Leu
310                85                    90                    95
313 Gly Gln Gln Pro Leu Pro Arg Arg Pro Gly His Asp Asp Gly Gln Arg
314                100                   105                   110
317 Pro Ser Gly Gly Ala Ala Ala Ala Pro Arg Arg Gly Ala Gln Leu Arg
318                115                   120                   125
321 Arg Pro Arg His Ser His Pro Thr Arg Ala Arg Arg Cys Pro Gly Gly
322                130                   135                   140
325 Leu Pro Gly His Ala Gly Gly Ala Ala Pro Gly Arg Gly Ala Ala Gly
326 145                150                   155                   160
329 Arg Ala Arg Cys Leu Gly Pro Ser Ala Arg Gly Pro Gly
330                165                   170
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335 <212> TYPE: DNA
336 <213> ORGANISM: Homo sapien
338 <400> SEQUENCE: 6
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343 gggcgcgctc aggaaggcg ggtgcgcgcc tgcggggcgg agatgggcag ggggcggtgc      180
345 gtgggtccca gtctgcagtt aagggggcag gagtggcgct gctcacctct ggtgccaaag      240
347 ggcggcgtag cggctgccga gctcggccct ggaggcggcg agaactgggt gcgcagggtc      300
349 ttggtgaccc tccggattcg gcgcgcgtgc ggcccgcgcg gagtgagggt tttcgtgggt      360
351 cacatcccgc ggctcacggg ggagtgggca gcgccagggg cgcccgcgcg tgtggccctc      420
353 gtgctgatgc tactgaggag ccagcgtcta gggcagcagc cgcttcctag aagaccaggt      480
355 catgatgatg ggcagcgccc gagtggcgga gctgctgctg ctccacggcg cggagcccaa      540
357 ctgcgccgac cccgccactc tcaccggacc cgtgcacgac gctgcccggg agggcttcct      600

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363 cgcggctgcg gggggcacca gaggcagtaa ccatgcccgc atagatgccg cggaagggtcc 780
365 ctcagacatc cccgattgaa agaaccagag aggcctctgag aaacctcggg aaacttagat 840
367 catcagtcac cgaaggctcct acagggccac aactgcccc gccacaaccc accccgcttt 900
369 cgtagttttc atttagaaaa tagagctttt aaaaatgtcc tgccttttaa cgtagatata 960
371 tgccttcccc cactaccgta aatgtccatt tatatcattt tttatatatt cttataaaaa 1020
373 tgtaaaaaag aaaaacaccg cttctgcctt ttcaactgtg tggagttttc tggagtgage 1080
375 actcacgccc taagcgcaca ttcatgtggg cattttctgc gagcctcgca gcctccggaa 1140
377 gctgtcgact tcatgacaag cattttgtga actagggaag ctcagggggg ttactggctt 1200
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384 &lt;210&gt; SEQ ID NO: 7

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386 &lt;212&gt; TYPE: PRT

387 &lt;213&gt; ORGANISM: Homo sapiens

389 &lt;400&gt; SEQUENCE: 7

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396 20 25 30
399 Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
400 35 40 45
403 Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val
404 50 55 60
407 Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg
408 65 70 75 80
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412 85 90 95
415 Ala Glu Gly Pro Ser Asp Ile Pro Asp
416 100 105

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429 ccgagtggcg gagctgctgc tgctccacgg cgcggagccc aactgcgccg accccgccac 180
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433 gcaccggggc ggggcggggc tggacgtgcg cgatgcctgg ggccgtctgc ccgtggacct 300
435 ggctgaggag ctgggccatc gcgatgtcgc acggtacctg cgcgcggctg cggggggcac 360
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445 taaatgtcca tttatatcat tttttatata ttcttataaa aatgtaaaaa agaaaaacac 660
447 cgcttctgcc ttttactgtg gttggagttt tctggagtga gcactcacgc cctaagcgca 720
449 cattcatgtg ggcatttctt gcgagcctcg cagcctccgg aagctgtcga cttcatgaca 780

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**VERIFICATION SUMMARY**

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